User Manual of JHU/KKI QSM_Toolbox_v3.0

Xu Li, PhD

Department of Radiology, Johns Hopkins University School of Medicine, Baltimore, MD, USA;

F.M. Kirby Research Center for Functional Brain Imaging, Kennedy Krieger Institute, Baltimore, MD, USA;

Introduction

JHU/KKI_QSM_Toolbox_v3.0 is a MATLAB software with graphic user interface (GUI) for doing Quantitative Susceptibility Mapping (QSM) processing from MR magnitude and phase data acquired with gradient echo sequence (GRE).

Installation

Since it is a MATLAB based toolbox, MATLAB installation is required. In addition, this toolbox also uses processing routine from FSL, e.g. bet, thus needs to have FSL installed.

Usage

1. To start, open MATLAB and go to the folder where this toolbox is installed.

2. run QSM.m, the GUI will show up.

3. Follow the procedures as described below.

3.1. Select the data file
Supported input file formats include: PAR/REC (Philips v4.2 and above), DICOM (Philips/GE/Siemens/Canon), EnhancedDICOM (Philips), .mat (MATLAB, customized, check "readerwrapper.m" under /QSM_Utilily/fileIO/ for details of this format)

Click
Select
Data
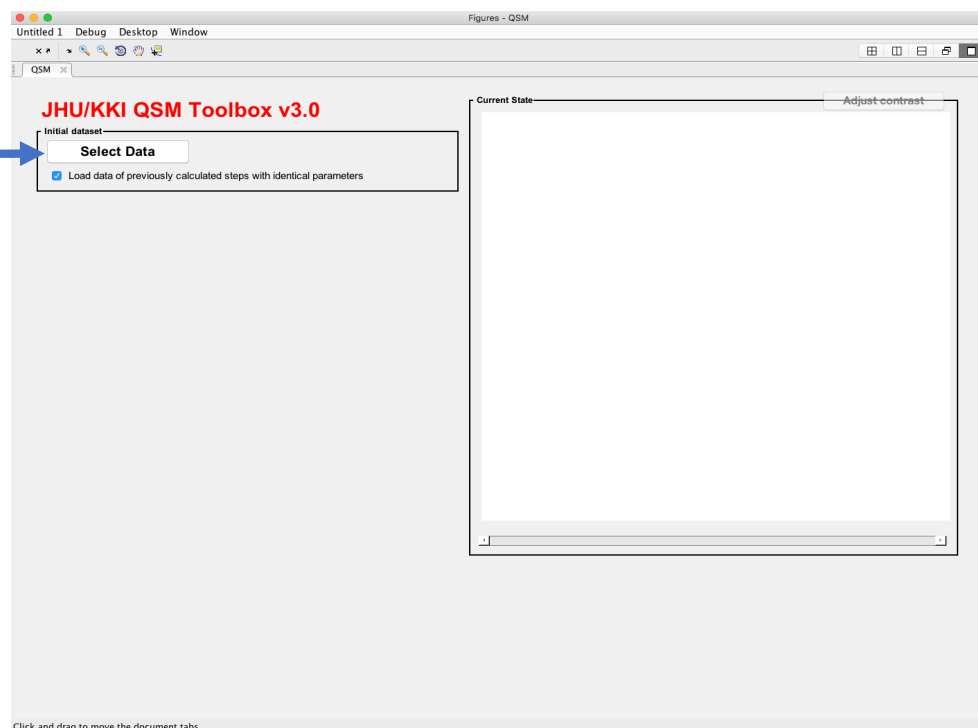
After the toolbox reads in the data, it shows some basic imaging acquisition parameters and the raw phase images.
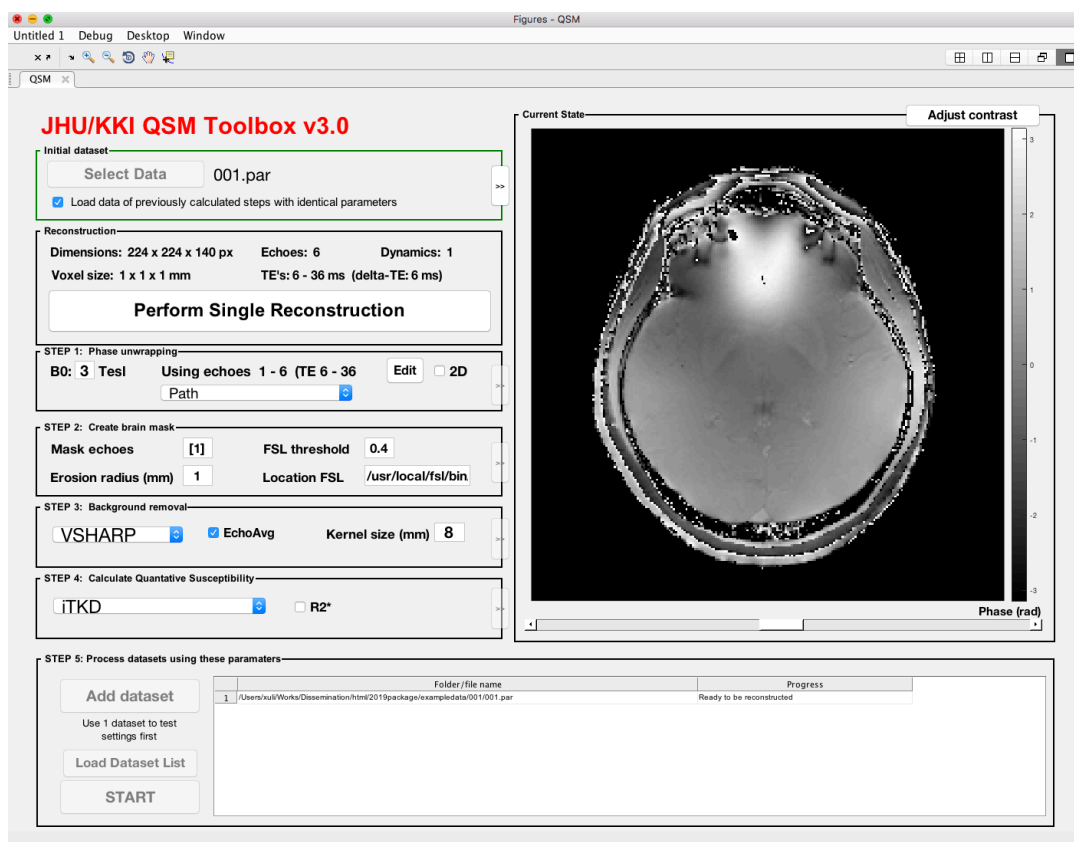
3.2 Select phase preprocessing and QSM methods and other parameters

Step 1:
a. Edit field strength if necessary
b. Select Echoes (Edit button)
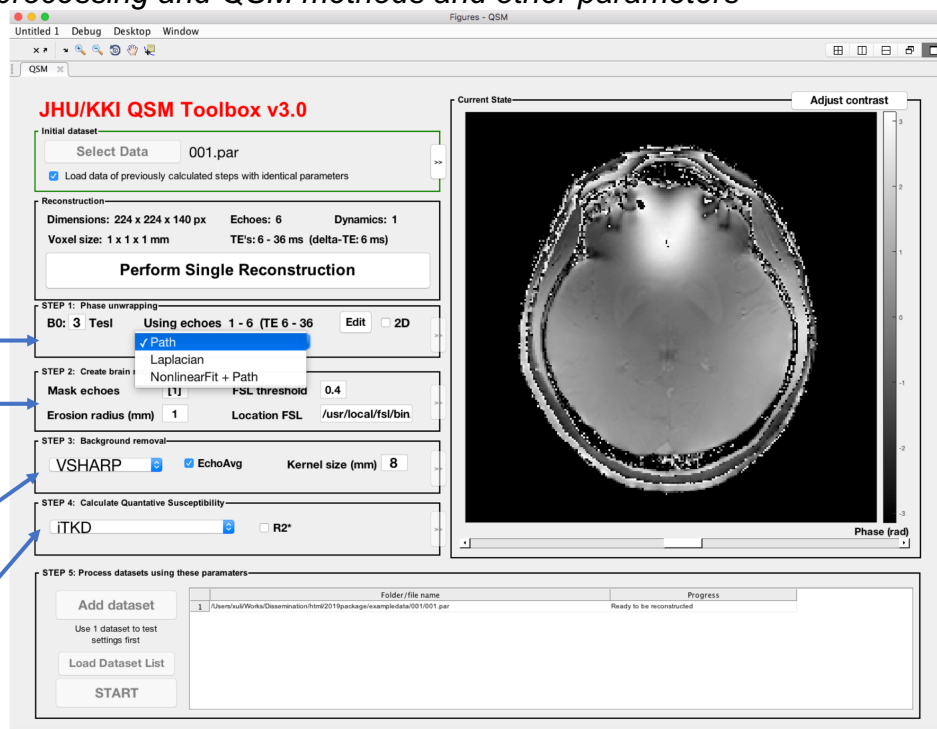c. Select phase unwrapping methods

Step 2:
a. Select echo and FSL BET parameters for brain masking

Step 3:
a. Select background field removal method

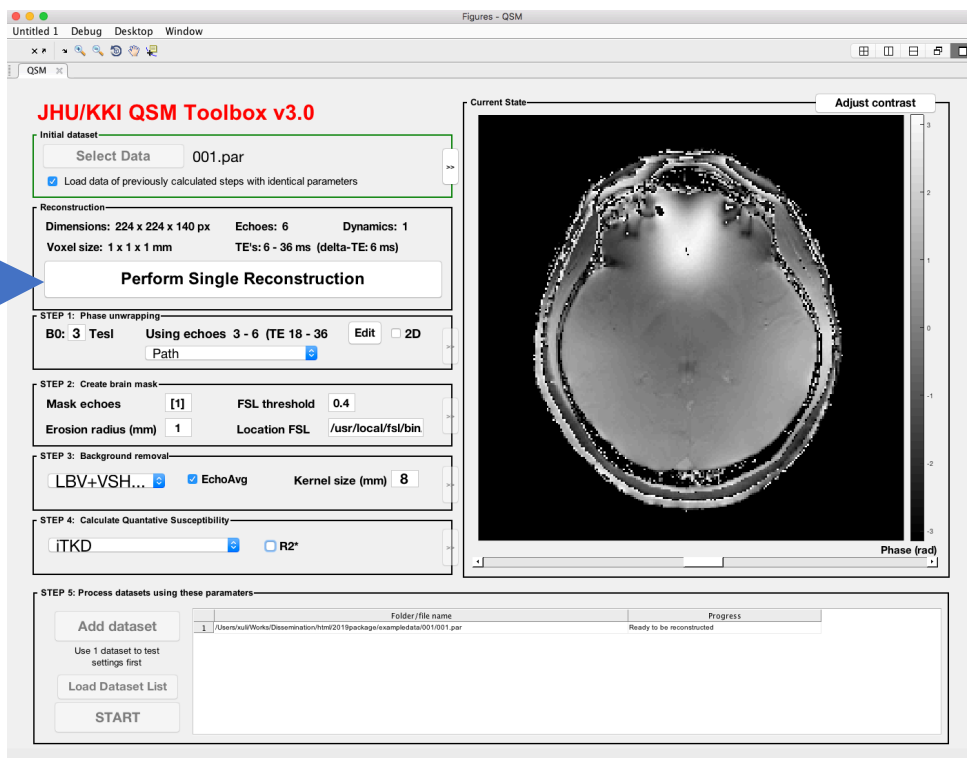**Step 4:**
a. Select QSM method
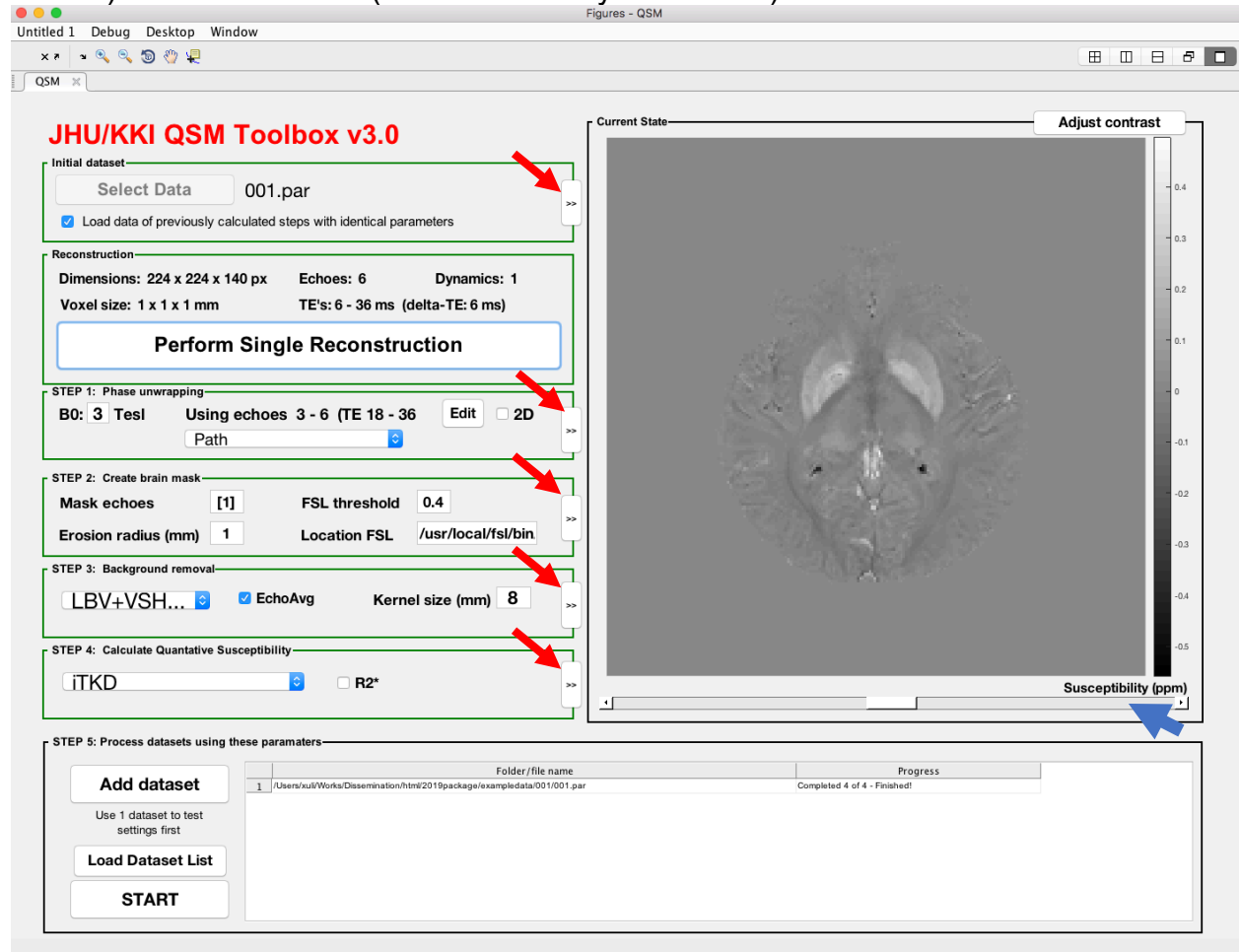
3.3 Start processing pipeline.

Click "Perform Single Reconstruction" to start the pipeline

3.4 Check results:

After QSM processing is finished, check the results of each step (buttons marked by red arrows) at different slices (slider marked by blue arrow).

Results are also output and saved in files in the data folder as following:

*_PhaseUnwrapped_echo3-6[Path/Lap/NLFPath].mat: Unwrapped phase (in radian) using [path/laplacian/nonlinear fitting+path] method, echo 3-6 (user-defined in step 3.2) was selected for QSM processing.

*GREMag#.nii.gz: GRE Magnitude Image of selected echo for brain masking

*GREMag#_brain.nii.gz: GRE Magnitude Image of brain only, using FSL BET

*GREMag#_brain_mask.nii.gz: brain mask from FSL BET

*_brain_mask_echo#_r#_t##.mat: final brain mask used for QSM

*[SMV/PDF/LBVSMV/iRSHARP]_[avg/LSlope/NLSlope]_echo3-6.mat:
Frequency map (in Hz) or local field map generated using
[VSHARP/PDF/LBV+VSHARP/iRSHARP] method, taking [echo averaging/linear fitting/nonlinear fitting], with echo3-6(user-defined). Have corresponding .nii.gz file too.

*R2star.mat/R2star.nii.gz: R2 star map (in Hz)

*chi_[iLSQR/TKD/iTKD/MEDI/SFCR/SFCR+0]:
QSM map (in ppm) calculated using different methods. Have corresponding .nii.gz file.

You can also change the parameters in phase preprocessing and QSM methods as shown in 3.2 and click "Perform Single Reconstruction" to test different settings and methods.

3.5 processing more data/batch processing

If satisfied with the results, you can load additional datasets to process using these settings by clicking "Add dataset", which will update the data list (red arrow). After adding all the data, click the "START" button to start batch processing.
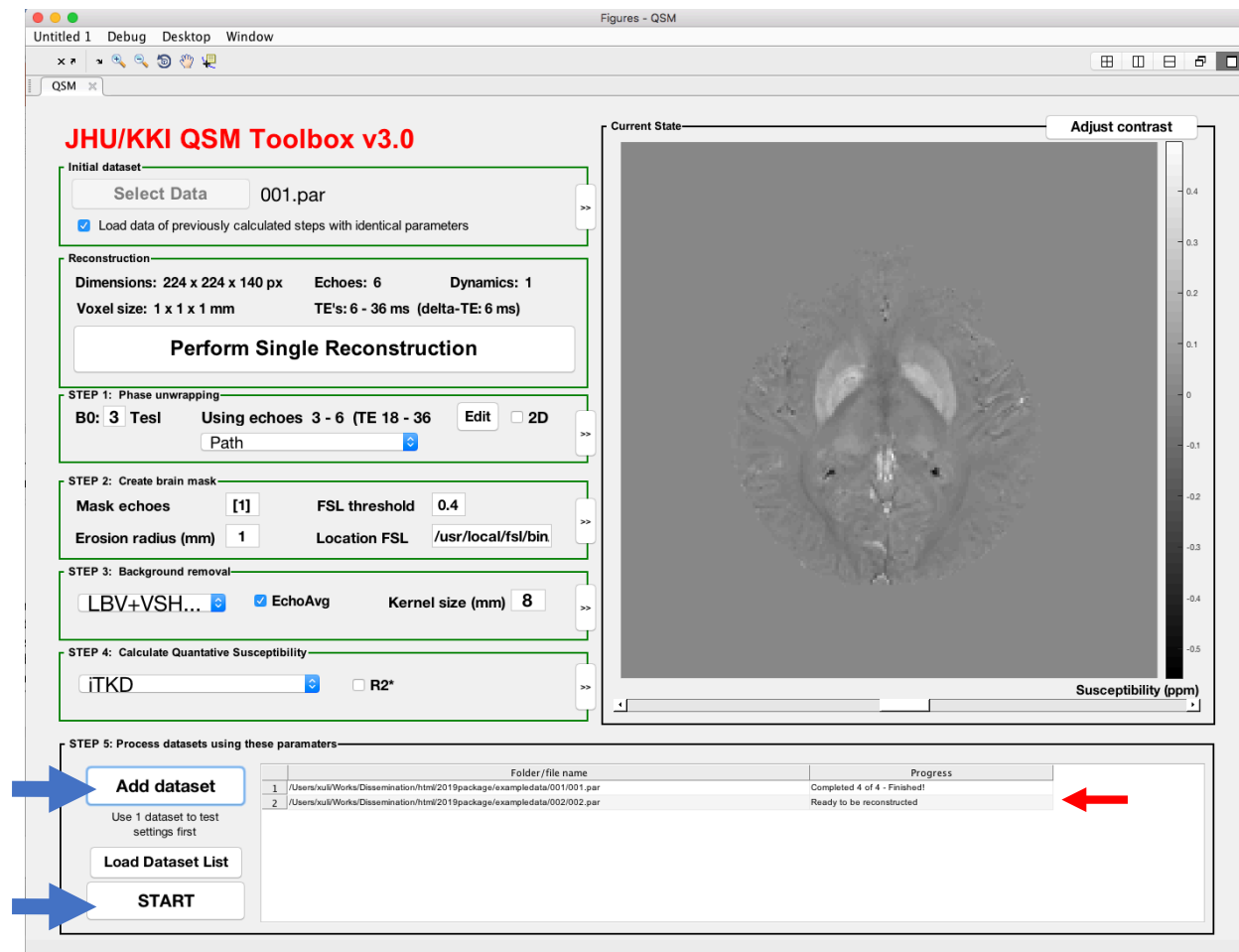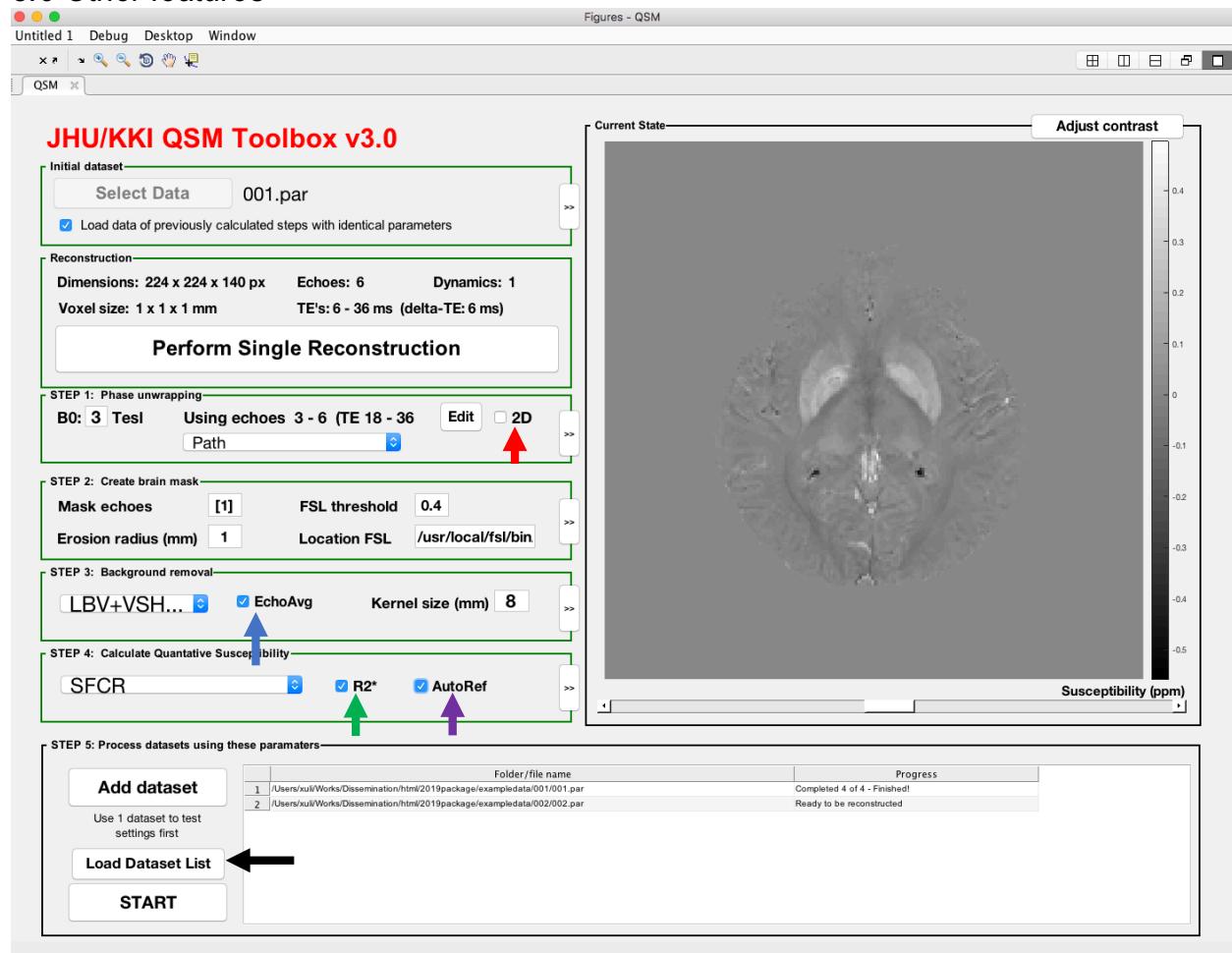
- 2D checkbox (red arrow): if checked, will perform 2D based Laplacian phase unwrapping and VSHARP on top of the 3D based methods. This may help improve QSM result derived from data acquired with 2D GRE sequence, but NOT guaranteed. This does NOT apply to other phase unwrapping and background removal pipelines.
- EchoAvg checkbox (blue arrow): if checked, MR phase data at different echoes will be averaged after phase unwrapping and background removal. If not checked, MR phase data will be fitted over echo time (TE) using either linear (default) or nonlinear way (if using "NonLinear Fit+Path" option for phase unwrapping).
- R2* checkbox: if checked, R2* map will be calculated using the ARLO method.
- AutoRef checkbox: if checked, QSM map automatically referenced to segmented CSF regions will be generated. This is ONLY available with multi-echo GRE data when R2* is calculated and using SFCR for QSM, giving SFCR+0 results.
- Load Dataset List button: This button can load a matlab .mat data file with variable "tableData" which is a cell array of datalist similar to the one created by using "Add dataset". This can be helpful for batch processing with large amount of data. See the "TestTable.mat" in the example data included in the package.

Contributions and Acknowledgements:

The main GUI of the JHU/KKI QSM Toolbox and pipelines are developed by Jiri van Bergen and Xu Li at Department of Radiology, Johns Hopkins University School of Medicine and F.M. Kirby Research Center for Functional Brain Imaging, Kennedy Krieger Institute, Baltimore, MD, USA. Contact via xuli@mri.jhu.edu.

Other contributors include:
Joseph Gillen, Craig Jones, Jonathan Farrell, Issel Lim and Jiadi Xu (Kirby Center @ KKI) and Lijun Bao, Jinsheng Fang (Xiamen University)

Some Codes are from or modifed from other publicly availabe codes including
 1. MEDI Toolbox: http://weill.cornell.edu/mri/pages/qsm.html
 2. Berkin Bilgic Software: http://martinos.org/~berkin/software.html

References to cite:

When using the toolbox, please cite some of our recent publications:
(Chen et al., 2019; Li et al., 2019; van Bergen et al., 2016)

- van Bergen, J.M., Hua, J., Unschuld, P.G., Lim, I.A., Jones, C.K., Margolis, R.L., Ross, C.A., van Zijl, P.C., Li, X., 2016. Quantitative Susceptibility Mapping Suggests Altered Brain Iron in Premanifest Huntington Disease. AJNR Am J Neuroradiol 37, 789-796.
- Chen, L., Hua, J., Ross, C.A., Cai, S., van Zijl, P.C.M., Li, X., 2019. Altered brain iron content and deposition rate in Huntington's disease as indicated by quantitative susceptibility MRI. J Neurosci Res 97, 467-479.
- Li, X., Chen, L., Kutten, K., Ceritoglu, C., Li, Y., Kang, N.D., Hsu, J.T., Qiao, Y., Wei, H.J., Liu, C.L., Miller, M.I., Mori, S., Yousem, D.M., van Zijl, P.C.M., Faria, A.V., 2019. Multi-atlas tool for automated segmentation of brain gray matter nuclei and quantification of their magnetic susceptibility. NeuroImage 191, 337-349.

In addition, please cite the corresponding publications related to each method as described below.

Phase Unwrapping Methods:

Best path based unwrapping (Abdul-Rahman et al., 2005)

- Abdul-Rahman, H., Gdeisat, M., Burton, D., Lalor, M., 2005. Fast three-dimensional phase-unwrapping algorithm based on sorting by reliability following a non-continuous path. Optical Metrology. International Society for Optics and Photonics, pp. 32-40.

Laplacian based phase unwrapping: (Li et al., 2011)

- Li, W., Wu, B., Liu, C., 2011. Quantitative susceptibility mapping of human brain reflects spatial variation in tissue composition. NeuroImage 55, 1645-1656.

Nonlinear fitting of phase evolution (Liu et al., 2013)
- Liu, T., Wisnieff, C., Lou, M., Chen, W., Spincemaille, P., Wang, Y., 2013. Nonlinear formulation of the magnetic field to source relationship for robust quantitative susceptibility mapping. Magn Reson Med 69, 467-476.

Background Removal Methods:
VSHARP (Schweser et al., 2011; Wu et al., 2012)
- Schweser, F., Deistung, A., Lehr, B.W., Reichenbach, J.R., 2011. Quantitative imaging of intrinsic magnetic tissue properties using MRI signal phase: an approach to in vivo brain iron metabolism? NeuroImage 54, 2789-2807.
- Wu, B., Li, W., Guidon, A., Liu, C., 2012. Whole brain susceptibility mapping using compressed sensing. Magn Reson Med 67, 137-147.

LBV (Zhou et al., 2014)
- Zhou, D., Liu, T., Spincemaille, P., Wang, Y., 2014. Background field removal by solving the Laplacian boundary value problem. NMR Biomed 27, 312-319.

PDF (Liu et al., 2011a)
- Liu, T., Khalidov, I., de Rochefort, L., Spincemaille, P., Liu, J., Tsiouris, A.J., Wang, Y., 2011a. A novel background field removal method for MRI using projection onto dipole fields (PDF). NMR Biomed 24, 1129-1136.

iRSHARP (Fang et al., 2019)
- Fang, J., Bao, L., Li, X., van Zijl, P.C.M., Chen, Z., 2019. Background field removal for susceptibility mapping of human brain with large susceptibility variations. Magn Reson Med 81, 2025-2037.

QSM methods:
TKD (Schweser et al., 2013; Shmueli et al., 2009)
- Shmueli, K., de Zwart, J.A., van Gelderen, P., Li, T.Q., Dodd, S.J., Duyn, J.H., 2009. Magnetic susceptibility mapping of brain tissue in vivo using MRI phase data. Magn Reson Med 62, 1510-1522.
- Schweser, F., Deistung, A., Sommer, K., Reichenbach, J.R., 2013. Toward online reconstruction of quantitative susceptibility maps: superfast dipole inversion. Magn Reson Med 69, 1582-1594.

iTKD (Aggarwal et al., 2018)
- Aggarwal, M., Li, X., Grohn, O., Sierra, A., 2018. Nuclei-specific deposits of iron and calcium in the rat thalamus after status epilepticus revealed with quantitative susceptibility mapping (QSM). J Magn Reson Imaging 47, 554-564.

iLSQR (Li et al., 2015)

- Li, W., Wang, N., Yu, F., Han, H., Cao, W., Romero, R., Tantiwongkosi, B., Duong, T.Q., Liu, C., 2015. A method for estimating and removing streaking artifacts in quantitative susceptibility mapping. NeuroImage 108, 111-122.

MEDI (Liu et al., 2012; Liu et al., 2011b)
- Liu, T., Liu, J., de Rochefort, L., Spincemaille, P., Khalidov, I., Ledoux, J.R., Wang, Y., 2011b. Morphology enabled dipole inversion (MEDI) from a single-angle acquisition: comparison with COSMOS in human brain imaging. Magn Reson Med 66, 777-783.
- Liu, J., Liu, T., de Rochefort, L., Ledoux, J., Khalidov, I., Chen, W., Tsiouris, A.J., Wisnieff, C., Spincemaille, P., Prince, M.R., Wang, Y., 2012. Morphology enabled dipole inversion for quantitative susceptibility mapping using structural consistency between the magnitude image and the susceptibility map. NeuroImage 59, 2560-2568.

SFCR (Bao et al., 2016; Langkammer et al., 2018)
- Bao, L., Li, X., Cai, C., Chen, Z., van Zijl, P.C., 2016. Quantitative Susceptibility Mapping Using Structural Feature Based Collaborative Reconstruction (SFCR) in the Human Brain. IEEE Trans Med Imaging 35, 2040-2050.
- Langkammer, C., Schweser, F., Shmueli, K., Kames, C., Li, X., Guo, L., Milovic, C., Kim, J., Wei, H., Bredies, K., Buch, S., Guo, Y., Liu, Z., Meineke, J., Rauscher, A., Marques, J.P., Bilgic, B., 2018. Quantitative susceptibility mapping: Report from the 2016 reconstruction challenge. Magn Reson Med 79, 1661-1673.

R2* method:
ARLO R2* method (Pei et al., 2015)
- Pei, M., Nguyen, T.D., Thimmappa, N.D., Salustri, C., Dong, F., Cooper, M.A., Li, J., Prince, M.R., Wang, Y., 2015. Algorithm for fast monoexponential fitting based on Auto-Regression on Linear Operations (ARLO) of data. Magn Reson Med 73, 843-850.